

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
- (ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 11-Jan-2000
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/899,437
(B) FILING DATE: 07/24/1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Conley, Deirdre L.
(B) REGISTRATION NUMBER: 36,487
(C) REFERENCE/DOCKET NUMBER: P1084R1C1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-2066
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2538 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ix) FEATURE:
(A) NAME/KEY: mouse NRG3 nucleic acid
(B) LOCATION: 1-2538
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50
TCGCGGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCTCCCCG 100
CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150
GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200
GCCCCGCCCC GCGCCCGCGC CCGGCCCGCG CGGCCCATG CCTCTGGCGC 250
GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300
GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350
CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GCGGCGGCG GCGGGGGGCC 400
CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCGGGA GTTACGCTGT 450
AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500
TCTGTTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550
GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCACGGA CCTGGTGGAC 600
TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650
CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700
CCACCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750
AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800
CCGGGTTCCC ATCCGGGCTA GCCGCGGCTC TACCACAGCA CGGAACACTG 850
CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTCTT CAGTAGCAGC 900
ACGCCCCGGT CCCGACCCC GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950
GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000
CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050
TCCTCCTCAC CCTCTTCCAC CTCCTCCACT ACCACCACCC CAGAAACTAG 1100
CACCAGCCCC AAATTTTATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150
ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200
GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCATAAGC ACTGTCGGTG 1250
CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300
ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTTAT GTATCATCTT 1400

TGGAATTGTC ATCGTGGGCA TGTTCGTGC AGCATTCTAC TTCAAAGCA 1450
 AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500
 AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
 GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600
 CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTC 1650
 CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
 CCCAGGACAA AGGAGTGGGA TGTTGCATAG GAATACTTTC AGAAGGGCAC 1750
 CACCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
 CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
 GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
 TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
 CAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
 TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050
 CCAATTCTGT GCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
 CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACTC 2150
 CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
 TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
 ATCCGGATTC TGA CTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
 CATGGAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350
 GTCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400
 ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450
 GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500
 TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
- (B) LOCATION: 1-713
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser
1 5 10 15
Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala
20 25 30
Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala
35 40 45
Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp
50 55 60
Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly
65 70 75
Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val
80 85 90
Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser
95 100 105
Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser
110 115 120
Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr
125 130 135
Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr
140 145 150
Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro
155 160 165
Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg
170 175 180
Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser
185 190 195
Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro
200 205 210
Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro
215 220 225
Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro
230 235 240
Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ala Ala Ser Ser
245 250 255
Ser Ser Pro Ser Ser Thr Ser Ser Thr Thr Thr Thr Pro Glu Thr
260 265 270
Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg
275 280 285

Ser	Glu	His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	
				290					295					300	
Leu	Asn	Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	
				305					310					315	
His	Lys	His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	
				320					325					330	
Asp	Gln	Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	
				335					340					345	
Asp	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Asp	Val	Tyr	Gln	
				350					355					360	
Arg	Gln	Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	
				365					370					375	
Val	Gly	Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	
				380					385					390	
Ala	Lys	Gln	Ile	Gln	Glu	His	Leu	Lys	Glu	Ser	Gln	Asn	Gly	Lys	
				395					400					405	
Asn	Tyr	Ser	Leu	Lys	Ala	Ser	Ser	Thr	Lys	Ser	Glu	Ser	Leu	Met	
				410					415					420	
Lys	Ser	His	Val	His	Leu	Gln	Asn	Tyr	Ser	Lys	Ala	Asp	Arg	His	
				425					430					435	
Pro	Val	Thr	Ala	Leu	Glu	Lys	Ile	Met	Glu	Ser	Ser	Phe	Ser	Ala	
				440					445					450	
Pro	Gln	Ser	Phe	Pro	Glu	Val	Thr	Ser	Pro	Asp	Arg	Gly	Ser	Gln	
				455					460					465	
Pro	Ile	Lys	His	His	Ser	Pro	Gly	Gln	Arg	Ser	Gly	Met	Leu	His	
				470					475					480	
Arg	Asn	Thr	Phe	Arg	Arg	Ala	Pro	Pro	Ser	Pro	Arg	Ser	Arg	Leu	
				485					490					495	
Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr	Gln	Gln	Leu	Glu	Glu	Ser	Arg	
				500					505					510	
Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro	Cys	Gln	Gly	Ile	Glu	Val	Arg	
				515					520					525	
Lys	Thr	Ile	Ser	His	Leu	Pro	Ile	Gln	Leu	Trp	Cys	Val	Glu	Arg	
				530					535					540	
Pro	Leu	Asp	Leu	Lys	Tyr	Val	Ser	Asn	Gly	Leu	Arg	Thr	Gln	Gln	
				545					550					555	
Asn	Ala	Ser	Ile	Asn	Met	Gln	Leu	Pro	Ser	Arg	Glu	Thr	Asn	Pro	
				560					565					570	

Tyr Phe Asn Ser Leu Asp Gln Lys Asp Leu Val Gly Tyr Leu Ser
 575 580 585
 Pro Arg Ala Asn Ser Val Pro Ile Ile Pro Ser Met Gly Leu Glu
 590 595 600
 Glu Thr Cys Met Gln Met Pro Gly Ile Ser Asp Val Lys Ser Ile
 605 610 615
 Lys Trp Cys Lys Asn Ser Tyr Ser Ala Asp Ile Val Asn Ala Ser
 620 625 630
 Met Pro Val Ser Asp Cys Leu Leu Glu Glu Gln Gln Glu Val Lys
 635 640 645
 Ile Leu Leu Glu Thr Val Gln Glu Gln Ile Arg Ile Leu Thr Asp
 650 655 660
 Ala Arg Arg Ser Glu Asp Phe Glu Leu Ala Ser Met Glu Thr Glu
 665 670 675
 Asp Ser Ala Ser Glu Asn Thr Ala Phe Leu Pro Leu Ser Pro Thr
 680 685 690
 Ala Lys Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile
 695 700 705
 Gln Arg Asp Ser Val Leu Thr Lys
 710 713

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mNRG3 extracellular domainAmino acid seq
- (B) LOCATION: 1-362
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser
 1 5 10 15
 Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala
 20 25 30
 Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala
 35 40 45
 Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp
 50 55 60

Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Pro	Thr	Val	Leu	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Pro	Gly	Ser	Arg	Pro	200	205	210
Pro	Met	Pro	Gly	Ala	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ala	Ala	Ser	Ser	245	250	255
Ser	Ser	Pro	Ser	Ser	Thr	Ser	Ser	Thr	Thr	Thr	Thr	Pro	Glu	Thr	260	265	270
Ser	Thr	Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	275	280	285
Ser	Glu	His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	290	295	300
Leu	Asn	Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	305	310	315
His	Lys	His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	320	325	330
Asp	Gln	Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	335	340	345

Asp His Leu Gly Ile Glu Phe Met Glu Ser Glu Asp Val Tyr Gln
 350 355 360

Arg Gln
 362

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn
 1 5 10 15
 Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys
 20 25 30
 His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln
 35 40 45
 Phe Leu
 47

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2502 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
- (B) LOCATION: 1-2502
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCACCGACCT AGTGGACTCC ACTAGGTCGG TGGGCACGTA CTCCTTGACG 50
 GAGCCCACCA CGATCCATTT GAGAAGCATG AGGCGCGGCC CCATGCCTCT 100
 GCCGCGGCCC TCGGGGGGGC GAAGGTGAAN ACCGGCTCCT AGGATGAGTG 150
 AAGGGGCGGC CGCTGCCTCG CCACCTGGTG CCGCTTCGGC AGCCGCCGCC 200

TCGGCCGAGG AGGGCACCGC GGCGGCTGCG GCGGCGGCAG CGGCGGGCGG 250
 GGGCCCGGAC GGCGGCGGCG AAGGGGCGGC CGAGCCCCC CGGGAGTTAC 300
 GCTGTAGCGA CTGCATCGTG TGGAACCGGC AGCAGACGTG GCTGTGCGTG 350
 GTACCTCTGT TCATCGGCTT CATCGGCCTG GGGCTCAGCC TCATGCTTCT 400
 CAAATGGATC GTGGTGGGCT CCGTCAAGGA GTACGTGCCC ACCGACCTAG 450
 TGGACTCCAA GGGGATGGGC CAGGACCCCT TCTTCCTCTC CAAGCCCAGC 500
 TCTTTCCCCA AGGCCATGGA GACCACCACC ACTACCACTT CCACCACGTC 550
 CCCC GCCACC CCCTCCGCCG GGGGTGCCGC CTCCTCCAGG ACGCCCAACC 600
 GGATTAGCAC TCGCCTGACC ACCATCACGC GGGCGCCAC TCGCTTCCCC 650
 GGGCACGGG TGCCCATCCG GGCCAGCCCG CGCTCCACCA CAGCACGGAA 700
 CACTGCGGCC CCTGCGACGG TCCCGTCCAC CACGGCCCCG TTCTTCAGTA 750
 GCAGCACGCT GGGCTCCCGA CCCC CGGTGC CAGGAACTCC AAGTACCCAG 800
 GCAATGCCCT CCTGGCCTAC TGCGGCATAC GCTACCTCCT CCTACCTTCA 850
 CGATTCTACT CCCTCCTGGA CCCTGTCTCC CTTTCAGGAT GCTGCCTCCT 900
 CTTCTTCCTC TTCTTCCTCC TCCGCTACCA CCACCACACC AGAAACTAGC 950
 ACCAGCCCCA AATTTTCATAC GACGACATAT TCCACAGAGC GATCCGAGCA 1000
 CTTCAAACCC TGCCGAGACA AGGACCTTGC ATACTGTCTC AATGATGGCG 1050
 AGTGCTTTGT GATCGAAACC CTGACCGGAT CCCATAAACA CTGTCGGTGC 1100
 AAAGAAGGCT ACCAAGGAGT CCGTTGTGAT CAATTTCTGC CGAAAACTGA 1150
 TTCCATCTTA TCGGATCCAA CAGACCACTT GGGGATTGAA TTCATGGAGA 1200
 GTGAAGAAGT TTATCAAAGG CAGGTGCTGT CAATTTTCATG TATCATCTTT 1250
 GGAATTGTCA TCGTGGGCAT GTTCTGTGCA GCATTCTACT TCAAAAGCAA 1300
 GAAACAAGCT AAACAAATCC AAGAGCAGCT GAAAGTGCCA CAAAATGGTA 1350
 AAAGCTACAG TCTCAAAGCA TCCAGCACAA TGGCAAAGTC AGAGAACTTG 1400
 GTGAAGAGCC ATGTCCAGCT GCAAAATTAT TCAAAGGTGG AAAGGCATCC 1450
 TGTGACTGCA TTGGAGAAAA TGATGGAGTC AAGTTTGTG GGGCCCCAGT 1500
 CATTCCTGA GGTCCCTTCT CCTGACAGAG GAAGCCAGTC TGTCAAACAC 1550
 CACAGGAGTC TATCCTCTTG CTGCAGCCCA GGGCAAAGAA GTGGCATGCT 1600
 CCATAGGAAT GCCTTCAGAA GGACACCCCC GTCACCCCGA AGTAGGCTAG 1650

GTGGAATTGT GGGACCAGCA TATCAGCAAC TCGAAGAATC AAGGATCCCA 1700
 GACCAGGATA CGATACCTTG CCAAGGGATA GAGGTCAGGA AGACTATATC 1750
 CCACCTGCCT ATACAGCTGT GGTGTGTTGA AAGACCCCTG GACTTAAAGT 1800
 ATTCATCCAG TGGTTTAAAA ACCCAACGAA ATACATCAAT AAATATGCAA 1850
 CTGCCTTCAA GAGAGACAAA CCCCTATTTT AATAGCTTGG AGCAAAAGGA 1900
 CCTGGTGGGC TATTCATCCA CAAGGGCCAG TTCTGTGCCC ATCATCCCTT 1950
 CAGTGGGTTT AGAGGAAACC TGCCTGCAAA TGCCAGGGAT TTCTGAAGTC 2000
 AAAAGCATCA AATGGTGCAA AAACCTCTAT TCAGCTGACG TTGTCAATGT 2050
 GAGTATTCCA GTCAGCGATT GTCTTATAGC AGAACAACAA GAAGTGAAAA 2100
 TATTGCTAGA AACTGTCCAG GAGCAGATCC GAATTCTGAC TGATGCCAGA 2150
 CGGTCAGAAG ACTACGAACT GGCCAGCGTA GAAACCGAGG ACAGTGCAAG 2200
 CGAAAACACA GCCTTTCTCC CCCTGAGTCC CACAGCCAAA TCAGAACGAG 2250
 AGGCGCAATT TGTCTTAAGA AATGAAATAC AAAGAGACTC TGCATTGACC 2300
 AAGTGACTTG AGATGTAGGA ATCTGTGCAT TCTATGCTTT GCTCAACAGG 2350
 AAAGAGAGGA AATCAAATAC AAATTATTTA TATGCATTAA TTTAAGAGCA 2400
 TCTACTTAGA AGAAACCAAA TAGTCTATCG CCCTCATATC ATAGTGTTTT 2450
 TTAACAAAAT ATTTTTTTAA GGGAAAGAAA TGTTTCAGGA GGGATAAAGC 2500
 TT 2502

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 amino acid sequence
- (B) LOCATION: 1-720
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser
1				5					10					15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala
				20					25					30

Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35					40					45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50					55					60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65					70					75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80					85					90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95					100					105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110					115					120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125					130					135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140					145					150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155					160					165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170					175					180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	
				185					190					195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	
				200					205					210	
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	
				215					220					225	
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	
				230					235					240	
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	
				245					250					255	
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr	
				260					265					270	
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu	
				275					280					285	
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn	
				290					295					300	
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys	
				305					310					315	

Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	Cys	Leu	Gln	Met	Pro	Gly	605	610	615
Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	Cys	Lys	Asn	Ser	Tyr	Ser	620	625	630
Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	Val	Ser	Asp	Cys	Leu	Ile	635	640	645
Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	Leu	Glu	Thr	Val	Gln	Glu	650	655	660
Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg	Arg	Ser	Glu	Asp	Tyr	Glu	665	670	675
Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser	Ala	Ser	Glu	Asn	Thr	Ala	680	685	690
Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys	Ser	Glu	Arg	Glu	Ala	Gln	695	700	705
Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg	Asp	Ser	Ala	Leu	Thr	Lys	710	715	720

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3 extracellular domain/Amino AcidSeq
- (B) LOCATION: 1-360
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	

Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser		95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser		110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr		125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr		140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro		155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg		170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser		185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro		200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro		215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro		230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser		245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr		260	265	270
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu		275	280	285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn		290	295	300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys		305	310	315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln		320	325	330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His		335	340	345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln		350	355	360

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn
1 5 10 15
Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys
20 25 30
His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln
35 40 45
Phe Leu
47

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: cARIA.egf
- (B) LOCATION: 1-48
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg
20 25 30
Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
35 40 45
Asn Tyr Val
48

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hAR.egf
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile His
1 5 10 15
Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys Lys
20 25 30
Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser Met
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hBTC.efg
(B) LOCATION: 1-45
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Ser Arg Cys Pro Lys Gln Tyr Lys His Tyr Cys Ile Lys
1 5 10 15
Gly Arg Cys Arg Phe Val Val Ala Glu Gln Thr Pro Ser Cys Val
20 25 30
Cys Asp Glu Gly Tyr Ile Gly Ala Arg Cys Glu Arg Val Asp Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hEGF.egf
(B) LOCATION: 1-46

[illegible][illegible]

01101101010101010101010101010101

01101101010101010101010101010101

01101101010101010101010101010101

[illegible][illegible]

01101101010101010101010101010101

01101101010101010101010101010101

[illegible]

01101101010101010101010101010101

[illegible][illegible][illegible][illegible][illegible][illegible]

01101101010101010101010101010101

[illegible]

01101101010101010101010101010101

01101101010101010101010101010101

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr
35 40 45
Glu Asn Tyr Pro
49

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHRGbeta.egf
- (B) LOCATION: 1-48
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
20 25 30
Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
35 40 45
Asn Tyr Val
48

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hTGFalpha.egf
- (B) LOCATION: 1-45
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

His Phe Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys Phe His
1 5 10 15
Gly Thr Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val
20 25 30

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(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 1
(B) LOCATION: 1-8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

Asn Asp Gly Glu Cys Phe Val Ile
1 5 8

(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(A) NAME/KEY: hNRG3B1 transmembrane proximal 2
(B) LOCATION: 1-9
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

Glu Phe Met Glu Ser Glu Glu Val Tyr
1 5 9

(A) LENGTH: 466 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(A) NAME/KEY: EST Genbank entry H23651
(B) LOCATION: 1-466
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

AATTTCTGCC	GAAAACTGAT	TCCATCTTAT	CGGATCCAAC	AGACCACTTG	50
GGGATTGAAT	TCATGGAGAG	TGAAGAAGTT	TATCAAAGGC	AGGTGCTGTC	100
AATTTTCATGT	ATCATCTTTG	GAATTGTCAT	CGTGGGCATG	TTCTGTGCAG	150

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SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2091 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(A) NAME/KEY: Human NRG3B2 (hNRGB2)
(B) LOCATION: 1-2091
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

107

ACCTTCACGA	TTCTACTCCC	TCCTGGACCC	TGTCTCCCTT	TCAGGATGCT	750
GCCTCCTCTT	CTTCCTCTTC	TTCCTCCTCC	GCTACCACCA	CCACACCAGA	800
AACTAGCACC	AGCCCCAAAT	TTCATACGAC	GACATATTCC	ACAGAGCGAT	850
CCGAGCACTT	CAAACCCTGC	CGAGACAAGG	ACCTTGCATA	CTGTCTCAAT	900
GATGGCGAGT	GCTTTGTGAT	CGAAACCCTG	ACCGGATCCC	ATAAACTG	950
TCGGTGCAA	GAAGGCTACC	AAGGAGTCCG	TTGTGATCAA	TTTCTGCCGA	1000
AAACTGATTC	CATCTTATCG	GATCCAACAG	ACCACTGGG	GATTGAATTC	1050
ATGGAGAGTG	AAGAAGTTTA	TCAAAGGCAG	GTGCTGTCAA	TTTCATGTAT	1100
CATCTTTGGA	ATTGTCATCG	TGGGCATGTT	CTGTGCAGCA	TTCTACTTCA	1150
AAAGCAAGAA	ACAAGCTAAA	CAAATCCAAG	AGCAGCTGAA	AGTGCCACAA	1200
AATGGTAAAA	GCTACAGTCT	CAAAGCATCC	AGCACAATGG	CAAAGTCAGA	1250
GAACTTGGTG	AAGAGCCATG	TCCAGCTGCA	AAATTATTCA	AAGGTGGAAA	1300
GGCATCCTGT	GACTGCATTG	GAGAAAATGA	TGGAGTCAAG	TTTTGTGCGC	1350
CCCCAGTCAT	TCCCTGAGGT	CCCTTCTCCT	GACAGAGGAA	GCCAGTCTGT	1400
CAAACACCAC	AGGAGTCTAT	CCTCTTGCTG	CAGCCCAGGG	CAAAGAAGTG	1450
GCATGCTCCA	TAGGAATGCC	TTCAGAAGGA	CACCCCGTC	ACCCCGAAGT	1500
AGGCTAGGTG	GAATTGTGGG	ACCAGCATAT	CAGCAACTCG	AAGAATCAAG	1550
GATCCCAGAC	CAGGATACGA	TACCTTGCCA	AGGGTATTCA	TCCAGTGGTT	1600
TAAAAACCCA	ACGAAATACA	TCAATAAATA	TGCAACTGCC	TTCAAGAGAG	1650
ACAAACCCCT	ATTTTAATAG	CTTGGAGCAA	AAGGACCTGG	TGGGCTATTC	1700
ATCCACAAGG	GCCAGTTCTG	TGCCATCAT	CCCTTCAGTG	GGTTTAGAGG	1750
AAACCTGCCT	GCAAATGCCA	GGGATTTCTG	AAGTCAAAAAG	CATCAAATGG	1800
TGCAAAAAC	CCTATTCAGC	TGACGTTGTC	AATGTGAGTA	TTCCAGTCAG	1850
CGATTGTCTT	ATAGCAGAAC	AACAAGAAGT	GAAAATATTG	CTAGAAACTG	1900
TCCAGGAGCA	GATCCGAATT	CTGACTGATG	CCAGACGGTC	AGAAGACTAC	1950
GAACGGGCA	GCGTAGAAAC	CGAGGACAGT	GCAAGTGAAA	ACACAGCCTT	2000
TCTCCCCCTG	AGTCCCACAG	CCAAATCAGA	ACGAGAGGCG	CAATTTGTCT	2050
TAAGAAATGA	AATACAAAGA	GACTCTGCAT	TGACCAAGTG	A 2091	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2
- (B) LOCATION: 1-696
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5					10					15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20					25					30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35					40					45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50					55					60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65					70					75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80					85					90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95					100					105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110					115					120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125					130					135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140					145					150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155					160					165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170					175					180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	
				185					190					195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	
				200					205					210	

Pro Val Pro Gly Thr	Pro Ser Thr Gln	Ala Met Pro Ser Trp	Pro
215		220	225
Thr Ala Ala Tyr	Ala Thr Ser Ser Tyr	Leu His Asp Ser Thr	Pro
230		235	240
Ser Trp Thr Leu	Ser Pro Phe Gln Asp	Ala Ala Ser Ser Ser	Ser
245		250	255
Ser Ser Ser Ser	Ser Ala Thr Thr Thr	Thr Pro Glu Thr Ser	Thr
260		265	270
Ser Pro Lys Phe	His Thr Thr Thr Tyr	Ser Thr Glu Arg Ser	Glu
275		280	285
His Phe Lys Pro	Cys Arg Asp Lys Asp	Leu Ala Tyr Cys Leu	Asn
290		295	300
Asp Gly Glu Cys	Phe Val Ile Glu Thr	Leu Thr Gly Ser His	Lys
305		310	315
His Cys Arg Cys	Lys Glu Gly Tyr Gln	Gly Val Arg Cys Asp	Gln
320		325	330
Phe Leu Pro Lys	Thr Asp Ser Ile Leu	Ser Asp Pro Thr Asp	His
335		340	345
Leu Gly Ile Glu	Phe Met Glu Ser Glu	Glu Val Tyr Gln Arg	Gln
350		355	360
Val Leu Ser Ile	Ser Cys Ile Ile Phe	Gly Ile Val Ile Val	Gly
365		370	375
Met Phe Cys Ala	Ala Phe Tyr Phe Lys	Ser Lys Lys Gln Ala	Lys
380		385	390
Gln Ile Gln Glu	Gln Leu Lys Val Pro	Gln Asn Gly Lys Ser	Tyr
395		400	405
Ser Leu Lys Ala	Ser Ser Thr Met Ala	Lys Ser Glu Asn Leu	Val
410		415	420
Lys Ser His Val	Gln Leu Gln Asn Tyr	Ser Lys Val Glu Arg	His
425		430	435
Pro Val Thr Ala	Leu Glu Lys Met Met	Glu Ser Ser Phe Val	Gly
440		445	450
Pro Gln Ser Phe	Pro Glu Val Pro Ser	Pro Asp Arg Gly Ser	Gln
455		460	465
Ser Val Lys His	His Arg Ser Leu Ser	Ser Cys Cys Ser Pro	Gly
470		475	480
Gln Arg Ser Gly	Met Leu His Arg Asn	Ala Phe Arg Arg Thr	Pro
485		490	495

Pro Ser Pro Arg Ser Arg Leu Gly Gly Ile Val Gly Pro Ala Tyr
 500 505 510
 Gln Gln Leu Glu Glu Ser Arg Ile Pro Asp Gln Asp Thr Ile Pro
 515 520 525
 Cys Gln Gly Tyr Ser Ser Ser Gly Leu Lys Thr Gln Arg Asn Thr
 530 535 540
 Ser Ile Asn Met Gln Leu Pro Ser Arg Glu Thr Asn Pro Tyr Phe
 545 550 555
 Asn Ser Leu Glu Gln Lys Asp Leu Val Gly Tyr Ser Ser Thr Arg
 560 565 570
 Ala Ser Ser Val Pro Ile Ile Pro Ser Val Gly Leu Glu Glu Thr
 575 580 585
 Cys Leu Gln Met Pro Gly Ile Ser Glu Val Lys Ser Ile Lys Trp
 590 595 600
 Cys Lys Asn Ser Tyr Ser Ala Asp Val Val Asn Val Ser Ile Pro
 605 610 615
 Val Ser Asp Cys Leu Ile Ala Glu Gln Gln Glu Val Lys Ile Leu
 620 625 630
 Leu Glu Thr Val Gln Glu Gln Ile Arg Ile Leu Thr Asp Ala Arg
 635 640 645
 Arg Ser Glu Asp Tyr Glu Leu Ala Ser Val Glu Thr Glu Asp Ser
 650 655 660
 Ala Ser Glu Asn Thr Ala Phe Leu Pro Leu Ser Pro Thr Ala Lys
 665 670 675
 Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile Gln Arg
 680 685 690
 Asp Ser Ala Leu Thr Lys
 695 696